IN THE CLAIMS

This complete listing of the pending claims replaces all previous listings of the claims.

1. (withdrawn) A method for in vitro detection of acute generalized inflammatory conditions (SIRS) in humans, comprising:

isolating sample RNA from a sample of body fluids from a human suspected of having SIRS;

labelling the sample RNA, and/or at least one DNA being a gene or gene fragment specific for sepsis, with a detectable label,

contacting the sample RNA with the DNA under hybridization conditions;

contacting control sample RNA representing a control for non-pathologic conditions with at least one DNA under hybridization conditions, wherein the DNA is a gene or gene fragment specific for SIRS, and wherein at least one of the control sample RNA and the DNA are labeled with a detectable label;

performing a quantitative detection of the label signals of the hybridized sample RNA and hybridized control sample RNA;

comparing the quantitative data of the label signals; and

in the case that the genes or gene fragments specific for SIRS are more expressed in the sample than in the control sample, diagnosing the mamal as having SIRS .

2. (currently amended) A method for in vitro diagnosis of sepsis and/or sepsis-like systemic inflammatory conditions or sepsis-like systemic infections in humans, comprising:

isolating sample RNA from a sample of body fluids from a human suspected of having sepsis or a sepsis like systemic inflammatory condition or sepsis-like systemic infection;

labelling (a) the sample RNA, and/or (b) at least one DNA being a gene or gene fragment specific for sepsis, with a detectable label;

contacting the sample RNA with the DNA under hybridization conditions;

contacting control sample RNA representing a control for non-pathologic conditions with at least one DNA under hybridization conditions, wherein the DNA is a gene or gene fragment specific for sepsis and/or sepsis-like systemic inflammatory conditions or sepsis-like systemic

infections, and wherein at least one of the control sample RNA and the DNA are labeled with a detectable label;

performing a quantitative detection of the label signals of the hybridized sample RNA and hybridized control sample RNA;

comparing the quantitative data of the label signals; and

in the case that the genes or gene fragments specific for sepsis and/or sepsis-like systemic inflammatory conditions or sepsis-like systemic infections are significantly over- or under-expressed in the sample than in the control sample, diagnosing the mamal as having sepsis and/or a sepsis-like systemic inflammatory condition or sepsis-like systemic infection.

3. (withdrawn) A method for in vitro detection of severe sepsis in humans, comprising:

isolating sample RNA from a sample of body fluids from a human suspected of having severe sepsis;

labelling the sample RNA, and/or at least one DNA being a gene or gene fragment specific for sepsis, with a detectable label,

contacting the sample RNA with the DNA under hybridization conditions;

contacting control sample RNA representing a control for non-pathologic conditions with at least one DNA under hybridization conditions, wherein the DNA is a gene or gene fragment specific for severe sepsis, and wherein at least one of the control sample RNA and the DNA are labeled with a detectable label;

performing a quantitative detection of the label signals of the hybridized sample RNA and hybridized control sample RNA;

comparing the quantitative data of the label signals; and

in the case that the genes or gene fragments specific for severe sepsis are significantly over- or under- expressed in the sample than in the control sample, diagnosing the mamal as having severe sepsis.

4. (previously presented) The method of claim 2, wherein the control RNA is hybridized with the DNA before the measurement of the sample RNA and the label signals of the control RNA/DNA-complex is gathered and, optionally, recorded in form of a calibration curve or table.

5. (previously presented) The method of claim 2, wherein genes which show the same expression level in healthy patients as well as in patients with sepsis and/or sepsis-like symptoms from sample and/or control RNA are used as reference genes for the quantification.

6. (previously presented) The method of claim 2, wherein mRNA is used as sample RNA.

7. (previously presented) The method of claim 2, wherein the DNA is arranged, immobilized, on predetermined areas on a carrier in the form of a microarray.

8. (withdrawn) The method of claim 1, wherein the method is used for at least one of:
early detection by means of differential diagnostics,
control of the clinical and therapeutic progress,
the individual risk evaluation in patients,
the evaluation whether the patient will respond to a specific treatment, and
post mortem diagnosis
of SIRS and/or sepsis and/or severe sepsis and/or systemic infections and/or septic conditions and/or infections.

9. (previously presented) The method of claim 2, wherein the body fluids are selected from the group consisting of blood, liquor, urine, ascitic fluid, seminal fluid, saliva, puncture fluid, cell content, and mixtures thereof.

10. (previously presented) The method of claim 9, wherein cell samples are subjected a lytic treatment, if necessary, in order to free their cell contents.

11. (canceled)

12. (currently amended) The method of claim 2, wherein the gene or gene segment specific for SIRS is selected from the group consisting of SEQ ID NO: III.1 to SEQ ID NO: III.4168, as well as gene fragments thereof with 20-2,000 [[5-2000]] or more nucleotides.

13. (currently amended) A method for in vitro diagnosis of sepsis and/or sepsis-like systemic inflammatory conditions and sepsis-like systemic infections in humans, comprising:

isolating sample RNA from a sample of body fluids from a human suspected of having sepsis or a sepsis like systemic inflammatory condition or sepsis-like systemic infection;

labelling the sample RNA, and/or at least one DNA being a gene or gene fragment specific for sepsis, with a detectable label;

contacting the sample RNA with the DNA under hybridization conditions;

contacting control sample RNA representing a control for non-pathologic conditions with at least one DNA under hybridization conditions, wherein the DNA is a gene or gene fragment specific for sepsis and/or sepsis-like conditions, and wherein at least one of the control sample RNA and the DNA are labeled with a detectable label;

performing a quantitative detection of the label signals of the hybridized sample RNA and hybridized control sample RNA;

comparing the quantitative data of the label signals; and

in the case that the genes or gene fragments specific for sepsis and/or sepsis-like systemic inflammatory conditions or sepsis-like systemic infection are significantly over- or under-expressed in the sample than in the control sample, diagnosing the human having sepsis and/or a sepsis-like condition, and

wherein the gene or gene segment specific for sepsis and/or sepsis-like conditions is selected from the group consisting of:

SEQ ID NO:	Patent Seq ID	Accession No
220	I.220	(AI540783)
303	I.303	(AI149693)
529	I.529	(AA280062)
754	I.754	(AA150160)
844	I.844	(AA035016)
1705	I.1705	(R70541)
2370	I.2370	(AI888493)
2449	I.2449	(AI821631)
2468	I.2468	(AI820576)
2481	I.2481	(AI811413)
2709	I.2709	(AI732517)
2831	I.2831	(AI675585)
2928	I.2928	(AI623567)
2948	I.2948	(AI613016)

3068	I.3068	(AI554111)
3079	I.3079	(AI539445)
3209	I.3209	(AI364529)
3268	I.3268	(AI343613)
3305	I.3305	(AI273261)
3317	I.3317	(AI281098)
3331	I.3331	(AI224886)
3399	I.3399	(AA868082)
3424	I.3424	(AA833528)
3433	I.3433	(AA812763)
3482	I.3482	(AI214494)
3508	I.3508	(AI221860)
3523	I.3523	(AI218498)
3624	I.3624	(AI217376)
3676	I.3676	(AI148246)
3765	I.3765	(AI041544)
3796	I.3796	(AI003843)
3873	I.3873	(AA947111)
3879	I.3879	(AA923246)
3881	I.3881	(AA923169)
3917	I.3917	(AA825968)
4060	I.4060	(AA708806)
4096	I.4096	(AA682790)
4122	I.4122	(AA478996)
4141	I.4141	(AA417348)
4268	I.4268	(AA417792)
4328	I.4328	(AA493225)
4450	I.4450	(AA495787)
4528	I.4528	(AA453996)
4609	I.4609	(AA412166)
4654	I.4654	(AA398757)
4695	I.4695	(AA035428)
4705	I.4705	(AA029887)
4937	I.4937	(W04695)
5265	I.5265	(H91663)
5338	I.5338	(H65331)
5418	I.5418	(R94894)
5542	I.5542	(H18649)
5567	I.5567	(H16790)
5647	I.5647	(H06263)
5779	I.5779	(R43301)
6018	I.6018	(R12411)
6200	I.6200	(T78484)
2393	I.2393	(AI866414)
2870	I.2870	(AI656486)
3760	I.3760	(AI023463)

2293	I.2293	(AI924733)
3704	I.3704	(AI147412)

, as well as gene fragments thereof with 20-2,000 ~~5-2000~~ nucleotides.

14. (currently amended) The method of claim 3, wherein the gene or gene segment specific for severe sepsis is selected from the group consisting of SEQ ID NO: II.1 to SEQ ID NO: II.130, as well as gene fragments thereof with 20-2,000 [[5-2000]] nucleotides.

15. (previously presented) The method of claim 2, wherein at least 2 to 100 different cDNAs are used.

16. (previously presented) The method of claim 2, wherein at least 200 different cDNAs are used.

17. (previously presented) The method of claim 2, wherein at least 200 to 500 different cDNAs are used.

18. (previously presented) The method of claim 2, wherein at least 500 to 1000 different cDNAs are used.

19. (previously presented) The method of claim 2, wherein at least 1000 to 2000 different cDNAs are used.

20. (previously presented) The method of claim 2, wherein the cDNA SEQ ID NO: III.1 to SEQ ID NO: III.4168, SEQ ID NO: I.1 to SEQ ID NO: I.6242 and SEQ ID NO: II.1 to SEQ ID NO: II.130 replaced by synthetic analoga as well as peptidonucleic acids.

21. (currently amended) The method of claim 20, wherein the synthetic analoga of the listed genes comprise 20-100 [[5-100]] base pairs.

22. (previously presented) The method of claim 2, wherein a radioactive label, in particular ^{32}P, ^{14}C, ^{125}I, ^{155}Eu, ^{33}P or ^{3}H is used as detectable label.

23. (previously presented) The method of claim 2, wherein a non-radioactive label is used selected from a color- or fluorescence label, an enzyme label or immune label, and/or quantum dots or a label with an electrically measurable signal characterized by at least one of change in potential, and/or conductivity and/or capacity by hybridizations.

24. (previously presented) The method of claim 2, wherein the sample RNA and control RNA bear the same label.

25. (previously presented) The method of claim 2, wherein the sample RNA and control RNA bear different labels.

26. (currently amended) The method of claim 7 [[2]], wherein the immobilized DNA ~~probes~~ bear a label.

27. (currently amended) The method of claim 15 [[2]], wherein the cDNA ~~probes~~ are immobilized on glass or plastics.

28. (currently amended) The method of claim 15 [[2]], wherein [[the]] individual cDNA molecules are immobilized on a ~~the~~ carrier material by means of a covalent binding.

29. (currently amended) The method of claim 15 [[2]], wherein the individual cDNA molecules are immobilized onto a ~~the~~ carrier material by means of adsorption selected from electrostatic, ~~and/or~~ dipole-dipole, ~~and/or~~ hydrophobic interactions and/~~or~~ hydrogen bridges.

30. (withdrawn) A method for in vitro detection of SIRS in humans, comprising:

isolating sample peptides from a sample of body fluids from a human suspected of having SIRS;

labelling of the sample peptides with a detectable label;

contacting the labelled sample peptides with at least one antibody or its binding fragment, whereby the antibody binds a peptide or peptide fragment specific for SIRS;

contacting labelled control peptides originating from healthy subjects with at least one antibody or its binding fragment immobilized on a carrier in the form of a microarray, whereby the antibody binds a peptide or peptide fragment specific for SIRS;

performing a quantitative detection of the label signals of the sample peptides and the control peptides;

comparing the quantitative data of the label signals in order determine whether the peptide or peptide fragments specific for SIRS are more expressed in the sample than in the control, and

in the case that the the peptide or peptide fragments specific for SIRS are significantly over- or under-expressed in the sample than in the control, diagnosing said human as aflicted with SIRS.

31. (withdrawn) A method for in vitro detection of sepsis and/or sepsis-like conditions in humans, comprising:

isolating sample peptides from a sample of body fluids from a human suspected of suffering from sepsis and/or sepsis-like conditions;

labelling of the sample peptides with a detectable label;

contacting labelled sample peptides with at least one antibody or its binding fragment, whereby the antibody binds a peptide or peptide fragment specific for sepsis and/or sepsis-like conditions;

contacting labelled control peptides stemming from healthy subjects with at least one antibody or its binding fragment immobilized on a carrier in the form of a microarray, whereby the antibody binds a peptide or peptide fragment specific for sepsis and/or sepsis-like conditions;

performing a quantitative detection of the label signals of the sample peptides and the control peptides; and

comparing the quantitative data of the label signals in order to determine whether the peptide or peptide fragments specific for sepsis and/or sepsis-like conditions are more expressed in the sample than in the control, and

in the case that the the peptide or peptide fragments specific for sepsis and/or sepsis-like conditions are significantly over- or under-expressed in the sample than in the control, diagnosing said human as aflicted with specific for sepsis and/or sepsis-like conditions.

32. (withdrawn) A method for in vitro detection of severe sepsis in humans, comprising:

isolating sample peptides from a sample of body fluids from a human suspected of suffering from severe sepsis;

labelling of the sample peptides with a detectable label;

contacting labelled sample peptides with at least one antibody or its binding fragment, whereby the antibody binds a peptide or peptide fragment specific for severe sepsis;

contacting labelled control peptides stemming from healthy subjects with at least one antibody or its binding fragment immobilized on a carrier in the form of a microarray, whereby the antibody binds a peptide or peptide fragment specific for severe sepsis;

performing a quantitative detection of the label signals of the sample peptides and the control peptides; and

comparing the quantitative data of the label signals in order to determine whether the peptide or peptide fragments specific for severe sepsis are more expressed in the sample than in the control, and

in the case that the the peptide or peptide fragments specific for severe sepsis are significantly over- or under-expressed in the sample than in the control, diagnosing said human as aflicted with severe sepsis.

33. (withdrawn) The method of claim 30, wherein the antibody is immobilized on an array in form of a microarray.

34. (withdrawn) The method of claim 30, wherein it is formed as immunoassay.

35. (withdrawn) The method of claim 30, wherein the method is used for at least one of:

early detection by means of differential diagnostics,

control of the clinical and therapeutic progress,

the individual risk evaluation in patients,

the evaluation whether the patient will respond to a specific treatment, and

post mortem diagnosis

of SIRS and/or sepsis and/or severe sepsis and/or systemic infections and/or septic conditions and/or infections.

36. (withdrawn) The method of claim 30, wherein the body fluid sample is selected from the following group: blood, liquor, urine, ascitic fluid, seminal fluid, saliva, puncture fluid, cell content, and mixtures thereof.

37. (withdrawn) The method of claim 30, wherein cell samples are subjected a lytic treatment, if necessary, in order to free their cell contents.

38. (canceled).

39. (withdrawn, currently amended) The method of claim 30, wherein the peptide specific for SIRS is an expression product of a gene or gene fragment selected from the group consisting of SEQ ID NO: III.1 to SEQ ID NO: III.4168, as well as gene fragments thereof with 20-2,000 [[5-2000]] nucleotides.

40. (withdrawn, currently amended) The method of claim 31, wherein the peptide specific for sepsis and/or sepsis-like conditions is an expression product of a gene or gene fragment selected from the group consisting of SEQ ID NO: I.1 to SEQ ID NO: I.6242, as well as gene fragments thereof with 20-2,000 [[5-2000]] nucleotides.

41. (withdrawn, currently amended) The method according to one of claim 32, wherein the peptide specific for severe sepsis is an expression product of a gene or gene fragment selected from the group consisting of SEQ ID NO: II.1 to SEQ ID NO: II.130, as well as gene fragments thereof with 20-2,000 [[5-2000]] nucleotides.

42. (withdrawn) The method of claim 30, wherein at least 2 to 100 different peptides are used.

43. (withdrawn) The method of claim 30, wherein at least 200 different peptides are used.

44. (withdrawn) The method of claim 30, wherein at least 200 to 500 different peptides are used.

45. (withdrawn) The method of claim 30, wherein at least 500 to 1000 different peptides are used.

46. (withdrawn) The method of claim 30, wherein at least 1000 to 2000 different peptides are used.

47. (withdrawn) The method of claim 30, wherein a radioactive label selected from ^{32}P, ^{14}C, ^{125}I, ^{155}Eu, ^{33}P and ^{3}H is used as detectable label.

48. (withdrawn) The method of claim 30, wherein a non-radioactive label is used as detectable label selected from a color- or fluorescence label, an enzyme label or immune label, and/or quantum dots or a label capable of being detected as an electrically measurable signal selected from the change in potential, and/or conductivity and/or capacity by hybridizations.

49. (withdrawn) The method of claim 30, wherein the sample peptides and control peptides bear the same label.

50. (withdrawn) The method of claim 30, wherein the sample peptides and control peptides bear different labels.

51. (withdrawn) The method of claim 30, wherein the probes used are peptides to which labelled antibodies are bound, which cause a change of signal of the labelled antibodies by change of conformation when binding to the sample peptides.

52. (withdrawn) The method of claim 30, wherein the peptide probes are immobilized on glass or plastics.

53. (withdrawn) The method of claim 30, wherein the individual peptide molecules are immobilized onto the carrier material by means of a covalent binding.

54. (withdrawn) The method of claim 30, wherein the individual peptide molecules are immobilized on the carrier material by means of adsorption by means of electrostatic and/or dipole-dipole and/or hydrophobic interactions and/or hydrogen bridges.

55. (withdrawn) The method of claim 30, wherein the individual peptide molecules are detected by means of monoclonal antibodies or their binding fragments.

56. (withdrawn) The method of claim 30, wherein the determination of individual peptides by means of immunoassay or precipitation assay is carried out using monoclonal antibodies.

57. (cancelled)

58. (cancelled)

59. (cancelled)

60. (currently amended) The method of claim 2, wherein the gene or gene segment specific for sepsis and/or sepsis-like conditions is selected from the group consisting of:

6250	II.8	(BC018761)
6251	II.9	(XM_030906)
6259	II.17	(NM_001562)
6267	II.25	(NM_001560)
6271	II.29	(XM_036107)
6297	II.55	(XM_041847)
6314	II.72	(NM_001511)
6327	II.85	(XM_007258)

as well as gene fragments thereof with 20-2,000 [[5-2000]] nucleotides.

61. (withdrawn, currently amended) The method of claim 2, wherein the gene or gene segment specific for sepsis and/or sepsis-like conditions is selected from the group consisting of SEQUENCE ID No. I.1 to SEQUECE ID No. I.6242, as well as gene fragments thereof with 20-2,000 [[5-2000]] nucleotides.